

#4

OIPE

## RAW SEQUENCE LISTING

DATE: 08/15/2001

PATENT APPLICATION: US/09/827,937A

TIME: 14:22:49

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5 <110> APPLICANT: Li, Yi
8   Ruben, Steven M.
13 <120> TITLE OF INVENTION: Human G-Protein Coupled Receptors
19 <130> FILE REFERENCE: 1488.1220003
25 <140> CURRENT APPLICATION NUMBER: 09/827,937A
28 <141> CURRENT FILING DATE: 2001-04-09
33 <150> PRIOR APPLICATION NUMBER: 08/852,824
36 <151> PRIOR FILING DATE: 1997-05-07
41 <160> NUMBER OF SEQ ID NOS: 18
47 <170> SOFTWARE: PatentIn Ver. 2.0
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56 <211> LENGTH: 2247
59 <212> TYPE: DNA
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93 ttaaaaggaa aataccagat gccactctgc aggctgcaat aactactact tactggatac 180
99 attcaaacc tccagaatca acagttatca ggtaaccaac aagaa atg caa gcc gtc 237
   Met Gln Ala Val
102
105
111 gac aat ctc acc tct gcg cct ggg aac acc agt ctg tgc acc aga gac 285
114 Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu Cys Thr Arg Asp
117   5              10              15              20
123 tac aaa atc acc cag gtc ctc ttc cca ctg ctc tac act gtc ctg ttt 333
126 Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr Thr Val Leu Phe
129              25              30              35
135 ttt gtt gga ctt atc aca aat ggc ctg gcg atg agg att ttc ttt caa 381
138 Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg Ile Phe Phe Gln
141              40              45              50
147 atc cgg agt aaa tca aac ttt att ttt ctt aag aac aca gtc att 429
150 Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys Asn Thr Val Ile
153              55              60              65
159 tct gat ctt ctc atg att ctg act ttt cca ttc aaa att ctt agt gat 477
162 Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys Ile Leu Ser Asp
165              70              75              80
171 gcc aaa ctg gga aca gga cca ctg aga act ttt gtg tgt caa gtt acc 525
174 Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val Cys Gln Val Thr
177   85              90              95              100
183 tcc gtc ata ttt tat ttc aca atg tat atc agt att tca ttc ctg gga 573
186 Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile Ser Phe Leu Gly
189              105              110              115
195 ctg ata act atc gat cgc tac cag aag acc acc agg cca ttt aaa aca 621
198 Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg Pro Phe Lys Thr

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210 Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu Ser Val Val Ile
213          135          140          145
219 tgg gca ttc atg ttc tta ctc tct ttg cct aac atg att ctg acc aac 717
222 Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met Ile Leu Thr Asn
225          150          155          160
231 agg cag ccg aga gac aag aat gtg aag aaa tgc tct ttc ctt aaa tca 765
234 Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser Phe Leu Lys Ser
237 165          170          175
243 gag ttc ggt cta gtc tgg cat gaa ata gta aat tac atc tgt caa gtc 813
246 Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr Ile Cys Gln Val
249          185          190          195
255 att ttc tgg att aat ttc tta att gtt att gta tgt tat aca ctc att 861
258 Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys Tyr Thr Leu Ile
261          200          205          210
267 aca aaa gaa ctg tac cgg tca tac gta aga acg agg ggt gta ggt aaa 909
270 Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg Gly Val Gly Lys
273          215          220          225
279 gtc ccc agg aaa aag gtg aac gtc aaa gtt ttc att atc att gct gta 957
282 Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile Ile Ile Ala Val
285          230          235          240
291 ttc ttt att tgt ttt gtt cct ttc cat ttt gcc cga att cct tac acc 1005
294 Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg Ile Pro Tyr Thr
297 245          250          255
303 ctg agc caa acc cgg gat gtc ttt gac tgc act gct gaa aat act ctg 1053
306 Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala Glu Asn Thr Leu
309          265          270          275
315 ttc tat gtg aaa gag agc act ctg tgg tta act tcc tta aat gca tgc 1101
318 Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser Leu Asn Ala Cys
321          280          285          290
327 ctg gat ccg ttc atc tat ttt ttc ctt tgc aag tcc ttc aga aat tcc 1149
330 Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser Phe Arg Asn Ser
333          295          300          305
339 ttg ata agt atg ctg aag tgc ccc aat tct gca aca tct ctg tcc cag 1197
342 Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr Ser Leu Ser Gln
345          310          315          320
351 gac aat agg aaa aaa gaa cag gat ggt ggt gac cca aat gaa gag act 1245
354 Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro Asn Glu Glu Thr
357 325          330          335          340
363 cca atg taaacaaatt aactaaggaa atatttcaat ctctttgtgt tcagaactcg 1301
366 Pro Met
372 ttaaagcaaa ggcctaagta aaaatattaa ctgacgaaga agcaactaag ttaataataa 1361
378 tgactctaaa gaaacagaag attacaaaag caattttcat ttacctttcc agtatgaaaa 1421
384 gctatcttaa aatatagaaa actaatctaa actgtagctg tattagcagc aaaacaaacg 1481
390 acatccaatt gtcatgctgc atgcaaaact acacagaatt catgttttgg cagagttttg 1541
396 gcaaaatgag taatcatata atatttactg taatttttaa aatacattat cgttcacaat 1601
402 tttatttttt cataatcaac taaggaagaa cgatcaattg gatataatct tcttaccaaa 1661
408 aatgatagtt aaaatgtata tatatcctag tcccctaacc aaatcctgac ctattgggat 1721

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426 ttatgtttat ttagaagata aagatttaag aagaccttta caataaagag aagaaatatac 1901
432 gaagtcatta aaataaggag acttactttt atgacattct aatactaaaa aatatagaaa 1961
438 tatttcctta attctagaga aactagtttt actaattttt tacaacttca ataataccat 2021
444 cactgacact taccttttatt aattagcttc tagaaaatag ctgctaatta ggttaatgaa 2081
450 cattttacct tagtgaaaaa aaattaatta aatatgatta caaagttgca cagcataact 2141
456 actgagagga aagtgattga tctgtttgta attacttggt tgtattggtg tgtataaaat 2201
462 acaaattttac attaaactct aaatcattaa aaaaaaaaaa aaaaaa 2247
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474 <211> LENGTH: 342
477 <212> TYPE: PRT
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498 Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
501 20 25 30
507 Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
510 35 40 45
516 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
519 50 55 60
525 Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
528 65 70 75 80
534 Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
537 85 90 95
543 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
546 100 105 110
552 Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
555 115 120 125
561 Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
564 130 135 140
570 Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
573 145 150 155 160
579 Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
582 165 170 175
588 Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
591 180 185 190
597 Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
600 195 200 205
606 Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
609 210 215 220
615 Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
618 225 230 235 240
624 Ile Ile Ala Val Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
627 245 250 255
633 Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
636 260 265 270
642 Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser

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645          275          280          285
651 Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
654          290          295          300
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735 Thr Gly Thr Pro Val Ala Pro Glu Ser Cys Gln Gln Leu Ala Ala Gly
738          5          10          15
744 ggg cac agc cgg ctc att gtt ctg cac tac aac cac tcg ggc cgg ctg 154
747 Gly His Ser Arg Leu Ile Val Leu His Tyr Asn His Ser Gly Arg Leu
750 20          25          30          35
756 gcc ggg cgc ggg ggg ccg gag gat ggc ggc ctg ggg gcc ctg cgg ggg 202
759 Ala Gly Arg Gly Gly Pro Glu Asp Gly Gly Leu Gly Ala Leu Arg Gly
762          40          45          50
768 ctg tcg gtg gcc gcc agc tgc ctg gtg gtg ctg gag aac ttg ctg gtg 250
771 Leu Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn Leu Leu Val
774          55          60          65
780 ctg gcg gcc atc acc agc cac atg cgg tcg caa cgc tgg gtc tac tat 298
783 Leu Ala Ala Ile Thr Ser His Met Arg Ser Gln Arg Trp Val Tyr Tyr
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792 tgc ctg gtg aac att acg atg agt gac ctg ctc acg ggc gcc gcc tac 346
795 Cys Leu Val Asn Ile Thr Met Ser Asp Leu Leu Thr Gly Ala Ala Tyr
798          85          90          95
804 ctg gcc aac gtg ctg ctg tcg ggg gcc cgc acc ttc cgt ctg gcg ccc 394
807 Leu Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg Leu Ala Pro
810 100          105          110          115
816 gcc cag tgg ttc cta cgg aag ggc ctg ctc ttc acc gcc ctg gcc gcc 442
819 Ala Gln Trp Phe Leu Arg Lys Gly Leu Leu Phe Thr Ala Leu Ala Ala
822          120          125          130
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834          135          140          145
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Input Set : A:\seqlist\_1488 1220003.txt

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846          150          155          160
852 ggc ttc atc ggc ctc tgc tgg ctg gcc gcg ctg ctg ggg atg ctg 586
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864 cct ttg ctg ggc tgg aac tgc ctg tgc gcc ttt gac cgc tgc tcc agc 634
867 Pro Leu Leu Gly Trp Asn Cys Leu Cys Ala Phe Asp Arg Cys Ser Ser
870 180          185          190
876 ctt ctg ccc ctc tac tcc aag cgc tac atc ctc ttc tgc ctg gtg atc 682
879 Leu Leu Pro Leu Tyr Ser Lys Arg Tyr Ile Leu Phe Cys Leu Val Ile
882          200          205          210
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891 Phe Ala Gly Val Leu Ala Thr Ile Met Gly Leu Tyr Gly Ala Ile Phe
894          215          220          225
900 cgc ctg gtg cag gcc agc ggg cag aag gcc cca cgc cca gcg gcc cgc 778
903 Arg Leu Val Gln Ala Ser Gly Gln Lys Ala Pro Arg Pro Ala Ala Arg
906          230          235          240
912 cgc aag gcc cgc cgc ctg ctg aag acg gtg ctg atg atc ctg ctg gcc 826
915 Arg Lys Ala Arg Arg Leu Leu Lys Thr Val Leu Met Ile Leu Leu Ala
918          245          250          255
924 ttc ttg gtg tgc tgg gga cca ctc ttc ggg ctg ctg ctg gcc gac gtc 874
927 Phe Leu Val Cys Trp Gly Pro Leu Phe Gly Leu Leu Leu Ala Asp Val
930 260          265          270          275
936 ttt ggc tcc aac ctc tgg gcc cag gag tac ctg cgg ggc atg gac tgg 922
939 Phe Gly Ser Asn Leu Trp Ala Gln Glu Tyr Leu Arg Gly Met Asp Trp
942          280          285          290
948 atc ctg gcc ctg gcc gtc ctc aac tcg gcg gtc aac ccc atc atc tac 970
951 Ile Leu Ala Leu Ala Val Leu Asn Ser Ala Val Asn Pro Ile Ile Tyr
954          295          300          305
960 tcc ttc cgc agc agg gag gtg tgc aga gcc gtg ctc agc ttc ctc tgc 1018
963 Ser Phe Arg Ser Arg Glu Val Cys Arg Ala Val Leu Ser Phe Leu Cys
966          310          315          320
972 tgc ggg tgt ctc cgg ctg ggc atg cga ggg ccc ggg gac tgc ctg gcc 1066
975 Cys Gly Cys Leu Arg Leu Gly Met Arg Gly Pro Gly Asp Cys Leu Ala
978          325          330          335
984 cgg gcc gtc gag gct cac tcc gga gct tcc acc acc gac agc tct ctg 1114
987 Arg Ala Val Glu Ala His Ser Gly Ala Ser Thr Thr Asp Ser Ser Leu
990 340          345          350          355
996 agg cca agg gac agc ttt cgc ggc tcc cgc tcg ctc agc ttt cgg atg 1162
999 Arg Pro Arg Asp Ser Phe Arg Gly Ser Arg Ser Leu Ser Phe Arg Met
1002          360          365          370
1008 cgg gag ccc ctg tcc agc atc tcc agc gtg cgg agc atc tgaagttgca 1211
1011 Arg Glu Pro Leu Ser Ser Ile Ser Ser Val Arg Ser Ile
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1032 tggacttgcc cgggtggcctc tcggggcttc tgacgccata tggacttgcc cattgcctat 1391
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1044 gtgtgggggc gagtgggttc cccacaaccc cgcttctgtg tgattctggg gaagtcccg 1511
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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/827,937A

DATE: 08/15/2001

TIME: 14:22:50

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Output Set: N:\CRF3\08152001\I827937A.raw

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